



Draft Genome Sequences of Two Multidrug-Resistant Sequence Type 405 *Escherichia coli* Isolates without Clinical Infection

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ABSTRACT We present the genome sequences of two carbapenemase-producing sequence type 405 *Escherichia coli* clinical isolates, strains Marseille-Q1950 and Marseille-Q1951. The isolates were obtained 1 month apart during the patient's hospitalization in Lebanon, in May (Marseille-Q1950) and June (Marseille-Q1951) 2019. The genome sizes of strains Marseille-Q1950 and Marseille-Q1951 were 5,181,515 bp and 5,213,451 bp, respectively.

We isolated two multidrug-resistant *Escherichia coli* strains, Marseille-Q1950 and Marseille-Q1951, from the same patient in May and June 2019, respectively, during his stay in the intensive care unit (ICU) at Saint George Hospital University Medical Center (SGHUMC) (Beirut, Lebanon). In May 2019, we obtained the first isolate when the patient's central femoral catheter was removed and sent for culture. In June 2019, we obtained the second isolate with a routine infection control surveillance and screening protocol in the SGHUMC ICU. The SGHUMC infection prevention and control division has a constitutional institutional review board waiver to retrieve relevant records for patients with pathogens of high importance.

The two samples were cultured on MacConkey agar for 24 h, incubated at 37°C, and then identified as *E. coli* by matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS). These two isolates were then used for genomic DNA extraction with the EZ1 BioRobot (Qiagen, Germany) using the EZ1 DNA tissue kit.

Antimicrobial susceptibility testing was performed on Mueller-Hinton agar by the disc diffusion method for all antimicrobials according to the EUCAST 2020 guidelines (https://www.eucast.org/fileadmin/src/media/PDFs/EUCAST_files/Breakpoint_tables/v_10.0_Breakpoint_Tables.pdf). Etest assays were additionally performed for ertapenem, imipenem, and fosfomycin. Among the tested antimicrobials, Marseille-Q1950 was susceptible only to fosfomycin, nitrofurantoin, and colistin. However, Marseille-Q1951 showed resistance to fosfomycin (Table 1). Interestingly, intravenous fosfomycin therapy is not available in Lebanon.

The genomic DNA of Marseille-Q1950 and Marseille-Q1951 was sequenced on the MiSeq platform (Illumina Inc., San Diego, CA, USA) by the paired-end strategy, as detailed previously (1, 2). The library was prepared following the workflow of the Nextera XT DNA library preparation kit (Illumina). Total information of 3.8 Gb was obtained with a cluster density of 416,000 clusters/mm², with 91.7% of clusters passing quality control filters. Within this run, the index representations for strains Marseille-Q1950 and Marseille-Q1951 were 3.16% and 6.9%, respectively. The 7,995,112 paired-end reads were quality filtered using FastQC v0.11.8 (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc>). We obtained 231,995 and 506,385 reads for strains Marseille-P1950 and Marseille-P1951, respectively. The forward and reverse strands were assembled using SPAdes v3.13 (3). Default parameters were used for

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TABLE 1 Antimicrobial susceptibility profiles of Marseille-Q1950 and Marseille-Q1951 according to EUCAST 2020 guidelines

Isolate	Antimicrobial susceptibility profile ^a															
	AMX	AMC	PTZ	KF	CRO	FEP	ETP	IPM	CT	AK	CN	CIP	FF	F	DO	TSX
Marseille-Q1950	R	R	R	R	R	R	32 µg/ml ^b	4 µg/ml ^b	S	R	R	R	S	S	R	R
Marseille-Q1951	R	R	R	R	R	R	32 µg/ml ^b	4 µg/ml ^b	S	R	R	R	192 µg/ml ^b	S	R	S

^a AMX, amoxicillin; AMC, amoxicillin-clavulanic acid; PTZ, piperacillin-tazobactam; KF, cephalothin; CRO, ceftriaxone; FEP, cefepime; ETP, ertapenem; IPM, imipenem; CT, colistin; AK, amikacin; CN, gentamicin; CIP, ciprofloxacin; FF, fosfomycin; F, nitrofurantoin; DO, doxycycline; TSX, trimethoprim-sulfamethoxazole; R, resistant; S, susceptible.

^b MIC determined by Etest assay.

all software. Marseille-Q1950 has a 5,181,515-bp-long genome assembled into 327 contigs (N_{50} 30,890 bp; L_{50} 50), with a G+C content of 50.44% and coverage of 13.36×. The genome of Marseille-Q1951 was assembled into 177 contigs (N_{50} 64,755 bp; L_{50} 22), with a size of 5,213,451 bp, coverage of 25.39×, and a G+C content of 50.46%. Genomic annotation was obtained using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.1 (4). A total of 5,076 genes were identified, along with 3 rRNAs and 51 tRNAs.

Using a multilocus sequence typing (MLST) tool (<https://github.com/tseemann/mlst>), sequence type 405 (ST405) was assigned to Marseille-Q1950 and Marseille-Q1951. Using ResFinder v4.1 (5), we identified the drug resistance genes *aadA2*, *bla*_{CTX-M-15}, *bla*_{NDM-5}, *bla*_{TEM-1B}, *catA1*, *dfrA12*, *rmtB*, *sulI*, and *tet(B)*. Using PlasmidFinder v2.1 (6) with an identity threshold of 95%, we identified plasmids in both isolates, i.e., Col(WS512), IncFIA, IncFIB(AP001918), and IncFII(pAMA1167-NDM-5). Using CARD (7) with an identity threshold of 95%, we identified the fosfomycin resistance mutations *mdtG*, *glpT* (E448K), and *cyaA* (S352T) only in Marseille-Q1951.

Data availability. The draft genome and read sequences have been deposited in GenBank (BioProject number [PRJNA697933](#)) under the following accession numbers: [JAFEVK000000000](#) and [SRR13578895](#) for strain Marseille-Q1950 and [JAFEVJ000000000](#) and [SRR13578894](#) for strain Marseille-Q1951.

REFERENCES

- Zgheib R, Anani H, Raoult D, Fournier P-E. 2020. Draft genome sequence of *Salirhabdus euzebyi* strain Q1438. *Microbiol Resour Announc* 9:e00246-20. <https://doi.org/10.1128/MRA.00246-20>.
- Kangale LJ, Zgheib R, Ghigo E, Raoult D, Fournier P-E. 2021. Draft genome sequence of *Herminiumonas contaminans* strain CCM 7991^T, a biopharmaceutical contaminant. *Microbiol Resour Announc* 10:e01432-20. <https://doi.org/10.1128/MRA.01432-20>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.
- Bortolaia V, Kaas RS, Ruppe E, Roberts MC, Schwarz S, Cattoir V, Philippon A, Allesoe RL, Rebelo AR, Florensa AF, Fagelhauer L, Chakraborty T, Neumann B, Werner G, Bender JK, Stengl K, Nguyen M, Coppens J, Xavier BB, Malhotra-Kumar S, Westh H, Pinholt M, Anjum MF, Duggett NA, Kempf I, Nykäsenoja S, Olkkola S, Wieczorek K, Amaro A, Clemente L, Mossong J, Losch S, Ragimbeau C, Lund O, Aarestrup FM. 2020. ResFinder 4.0 for predictions of phenotypes from genotypes. *J Antimicrob Chemother* 75:3491–3500. <https://doi.org/10.1093/jac/dkaa345>.
- Carattoli A, Zankari E, García-Fernández A, Voldby Larsen M, Lund O, Villa L, Moller Aarestrup F, Hasman H. 2014. In silico detection and typing of plasmids using PlasmidFinder and plasmid multilocus sequence typing. *Antimicrob Agents Chemother* 58:3895–3903. <https://doi.org/10.1128/AAC.02412-14>.
- Alcock BP, Raphenya AR, Lau TTY, Tsang KK, Bouchard M, Edalatmand A, Huynh W, Nguyen A-LV, Cheng AA, Liu S, Min SY, Miroshnichenko A, Tran H-K, Werfalli RE, Nasir JA, Oloni M, Speicher DJ, Florescu A, Singh B, Falty M, Hernandez-Koutoucheva A, Sharma AN, Bordeleau E, Pawlowski AC, Zubyk HL, Dooley D, Griffiths E, Maguire F, Winsor GL, Beiko RG, Brinkman FSL, Hsiao WWL, Domselaar GV, McArthur AG. 2020. CARD 2020: antibiotic resistance surveillance with the comprehensive antibiotic resistance database. *Nucleic Acids Res* 48: D517–D525. <https://doi.org/10.1093/nar/gkz935>.